IDT5-012 | Physiological and genetic insights towards understanding the canopy architecture in contrasting leaf size mutants of an upland size-Nagina 22 (N22)

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A set of contrasting leaf size mutants were identified from a stabilized population of EMS induced *Nagina-22* mutants. Phenotypically, these mutants differ for canopy architecture traits such as leaf number, leaf length and width, vein density and leaf angle. Owing to low leaf size and, hence, reduced canopy cover, the narrow leaf mutant (NL, N22_BADT_380_4) had reduced light interception compared to broad leaf mutant (BL, N22_BADT_437_1) and the wild type N22. The BL had high rate of shoot growth and low moisture retention capacity. However, the decreased leaf size of NL was compensated by increased leaf number, so that there was no difference in total leaf area (1540 and 1600 cm2.pl-1 respectively for NL and BL). Gas exchange analysis under two different water regimes revealed differences in photosynthetic and stomatal behaviour.The intrinsic WUE calculated by A/gs was high in narrow leaf mutant both under well watered (100% FC) and water limited (70% FC) condition. A MUTMAP population was developed by crossing NL with the wild type N22. The F2 population showed significant variability for the measured leaf traits. LL/LW ratio dramatically varied from 2.6 to 78.6 and the total leaf area ranged from 79 to 3544 cm2.pl-1. Anatomical features such as minor vein frequency per major veins was determined. The wild type had six while NL had four veins between the major veins. A significant diversity was also noticed among the MUTMAP population, which ranged between four and nine. However, the number of veins per unit distance ranged from 6 to 10.5. The population had significant correlation between seed weight and total leaf area, indicating the necessity of canopy architecture in determining crop yield.

IDT5-013 | QTL mapping for root architecture and transpiration efficiency in a maize introgression library

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High transpiration efficiency (TE) is one way to optimize water use. Although variation for root morpho-physiological traits can strongly affect the water status of a plant, the relationship between root traits and TE is not well understood. A maize introgression library (IL) derived from the cross between Gaspé Flint (an early line; donor parent) and B73 (an elite line; recurrent parent) were evaluated in order to identify QTLs for root system architecture (RSA), total biomass (TB), leaf area (LA), transpiration rate (TR), transpiration efficiency (TE), flowering time (FT), grain yield (GY) and yield components (YC). Two different experiments were carried out in order to study the genetic control of i) RSA, FT, GY and YC in response to drought in field conditions, at UNIBO, Italy and ii) TE, TR, TB and LA in controlled environment at different VPD, at ICRISAT, India. Differences in leaf area among the IL lines explained only 40% of the transpiration differences under high evaporative demand. QTLs were identified for all investigated traits. Overlaps between root and transpiration-related QTLs were detected on chromosomes 1 and 8. At these QTLs, the Gaspè Flint allele was associated with a TE decrease. A particularly interesting QTL for GY and YC, FT and TR was mapped on chromosome 3 (bin 3.3) where the Gaspè Flint allele was associated with an increase of both yield and transpiration rate and earliness.